GAU 1644

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of: Goodman et al.

Serial No. 08/971,172

Filed: November 14, 1997

For: *Robo: A Novel Family of Polypeptides and Nucleic Acids*

OIPE JC18 FEB 16 2000 PATENT & TRADEMARK OFFICE

Group Art Unit: 1644

Examiner: S. Turner

Attorney Docket No. B98-006-2

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CERTIFICATE OF MAILING
I hereby certify that this correspondence is being deposited with the United States Postal Service as First Class Mail in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 on February 7, 2000.

Signed _____
Richard Osman

RESPONSE

The Assistant Commissioner for Patents
Washington, DC 20231

Dear Commissioner:

Thank you for the action mailed Jan 21, 2000.

35USC112, second paragraph.

The phrase "flanked by fewer than 500 bp of native flanking sequence" is clear and definite to those of ordinary skill in the art in view of the specification. For example, on p.19, lines 27-33 the specification explains: "The subject recombinant nucleic acids comprising the nucleotide sequence of SEQ ID NO:1, 3, 5, 7, 9 or 11, or fragments thereof, contain such sequence or fragment at a terminus, immediately flanked by (i.e. contiguous with) a sequence other than that which it is joined to on a natural chromosome, or flanked by a native flanking region fewer than ... 500 bp, which is at a terminus or is immediately flanked by a sequence other than that which it is joined to on a natural chromosome."

This usage clearly conveys to those skilled in the art that (a) a strand "flanked by fewer than 500 bp of native flanking sequence" is contiguous with, on at least one end, fewer than 500 bp of native flanking sequence; (b) fewer than 500 bp includes zero bp and (c) native flanking sequence is sequence to which the strand is joined on a natural chromosome. Furthermore, native flanking sequences are readily determined from corresponding natural chromosome sources, which are identified in the specification (e.g. p.4, lines 1-3). The enclosed 132 Declaration demonstrates that one of ordinary skill in the relevant art finds the claims definite as pending. In any event, Applicants would be pleased to amend the claims in any equivalent manner preferred by the Examiner.

35USC102.

Wilson et al. discloses a 2.2 Mb sequence from chromosome III of C. elegans - representing about 2% of the C. elegans genome. Neither SEQ ID NO:05, nor SEQ ID NO:06 nor any closely related sequence appears in Wilson. In fact, the natural robo homolog in C. elegans is not even on chromosome III, but rather is on the X chromosome.

What the Examiner appears to rely on is a sequence deposit, designated O01632. O01632 is identical in sequence to EMBL/GenBank amino acid entry 1825710, which was generated and submitted by the same authors, but was reportedly released earlier, on Apr 21, 1997. 1825710 (and O01632) appear to encode residues 424-1297 of our SEQ ID NO:6.

Also on Apr 21, 1997, Genbank reportedly released U88183 and 1825711. U88183 (record appended below) is the sequence of X chromosome cosmid ZK377 and its annotation includes predicted open reading frames, including 1825710 and 1825711. 1825711 appears to encode residues 1-423 of SEQ ID NO:6. Hence, the sequence of natural C. elegans robo (SEQ ID NO:6, also known as sax-3, see p.28, line 3 of our specification) comprises a recombination of 1825710 and 1825711. Note that the annotation reference to the Wilson (1994) reference describing a chromosome III cosmid is not for any X chromosome sequence, but merely for methods used to sequence large parts of C. elegans chromosomes.

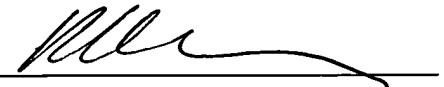
To the extent that the sequences of the 1825710 and 1825711 predicted reading frames are citeable art under 35USC102(a), the accompanying Declaration under 37CFR1.131 demonstrates that Applicants had possession of the claimed subject matter prior to their publication. Specifically, the Declaration shows that the full-length sequence encoding C. elegans robo (SEQ ID NO:6) was determined by Applicants prior to the April 21, 1997 publication dates of 1825710 and 1825711.

Upon allowability of the product claims of Group II, Applicants request joinder of method claims 43-49 (in the case of an elected product claim, rejoinder will be permitted when a product claim is found allowable and the withdrawn process claim depends from or otherwise includes all the limitations of an allowed product claim, per Commissioner Lehman's Notice of February 28, 1996: Guidance on Treatment of Product and Process Claims in light of In re Ochiai, In re Brouwer and 35 U.S.C. 103(b)).

We petition for any necessary extension of time (small entity) pursuant to 37 CFR 1.136(a). The Commissioner is hereby authorized to charge any fees or credit any overcharges associated with this communication to our Deposit Account No. 19-0750 (order no. B98-006-2).

The undersigned would by pleased to consider any further clarifying amendments sought by the Examiner and invites the Examiner to contact the undersigned by phone.

Respectfully submitted,
SCIENCE & TECHNOLOGY LAW GROUP



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>: U88183 . Caenorhabditis ele...[gi:1825708]
> PubMed, Protein, Related Sequences, Genome, LinkOut
>
> LOCUS CELZK377 32786 bp DNA INV
> 21-APR-1997
> DEFINITION Caenorhabditis elegans cosmid ZK377.
> ACCESSION U88183
> NID g1825708
> VERSION U88183.1 GI:1825708
> KEYWORDS .
> SOURCE Caenorhabditis elegans strain=Bristol N2.
> ORGANISM Caenorhabditis elegans
> Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia;
> Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae;
> Caenorhabditis.
> REFERENCE 1 (bases 1 to 32786)
> AUTHORS Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
> Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
> Coulson,A., Craxton,M., Dear,S., Du,Z., Durbin,R., Favello,A.,
> Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
> Johnston,L., Jones,M., Kershaw,J., Kirsten,J., Laister,N.,
> Latreille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
> O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
> Saunders,D., Shownkeen,R., Smaldon,N., Smith,A., Sonnhammer,E.,
> Staden,R., Sulston,J., Thierry-Mieg,J., Thomas,K., Vaudin,M.,
> Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
> Wilkinson-Sproat,J. and Wohldman,P.
> TITLE 2.2 Mb of contiguous nucleotide sequence from
> chromosome III of C. elegans
> JOURNAL Nature 368 (6466), 32-38 (1994)
> MEDLINE 94150718
> REFERENCE 2 (bases 1 to 32786)
> AUTHORS Nhan,M and Hawkins,J.
> TITLE The sequence of C. elegans cosmid ZK377
> JOURNAL Unpublished (1997)
> REFERENCE 3 (bases 1 to 32786)
> AUTHORS Waterston,R.
> TITLE Direct Submission
> JOURNAL Submitted (03-FEB-1997)
> REFERENCE 4 (bases 1 to 32786)
> AUTHORS Waterston,R.
> TITLE Direct Submission
> JOURNAL Submitted (21-APR-1997)
> COMMENT Submitted by:
> Genome Sequencing Center
> Department of Genetics, Washington University,
> St. Louis, MO 63110, USA, and
> Sanger Centre, Hinxton Hall
> Cambridge CB10 IRQ, England
> e-mail: rw@nematode.wustl.edu and
> jes@sanger.ac.uk
> NOTICE: This sequence may not be the entire insert of
> this clone.
> It may be shorter because we only sequence overlapping

> sections once, or longer because we provide a small
> overlap between neighboring submissions.
>
> This sequence was finished as follows unless otherwise
> noted:
> all regions were double stranded or sequenced with an
> alternate chemistry; an attempt was made to resolve all
> sequencing problems, as compressions and repeats; all
> regions were covered by sequence from more than one
> subclone.
>
> NEIGHBORING COSMID INFORMATION:
>
> The 5' cosmid is ZK813, 1500 bp overlap;3' cosmid is
> C12D12, 500 bp overlap. Actual start of this cosmid is at
> base position 1497 of CELZK377; actual end is at 8302 of
> CELC12D12
>
> NOTES:
> Coding sequences below are predicted from computer
> analysis, using the program Genefinder(P. Green and L.
> Hillier, ms in preparation).
> FEATURES Location/Qualifiers
> source 1..32786
> /organism="Caenorhabditis elegans"
> /strain="Bristol N2"
> /db_xref="taxon:6239"
> /chromosome="X"
> /clone="ZK377"
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> CDS
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> 1953..2240,2294..3087,3146..3417))
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>coded for by
> C. elegans cDNA yk142c5.5"
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> /db_xref="GI:1825710"
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>KNEDGESTWSASLTVEDHTSNAQFVRMPDPSNFPSSPTQPIIVNVTDTEVELHWNAPS
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>WKKRKLEELIDGYYIKWRGPPRTNDNQYVNVTSPSTENYVVSNLMPFTNYEFFVIPYH
>SGVHSIHGAPSNSMDVLTAEAPPSLPPEDVRIRMLNLTTLRISWKAPKADGINGILKG
>FQIVIVGQAPNNNRNITTNERAASVTLFHLVTGMTYKIRVAARSNGGVGVSHGTSEVI
>MNQDTLEKHLAAQQENESFLYGLINKSHVPVIVIVAILIIFVVIIIAYCYWRNSRNSD
>GKDRSFIKINDGSVHMASNNLWDVAQNPNQNPMYNTAGRMTMNNRNGQALYSLTPNAQ
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>GGHVYDTATRRQLNRGSTPREDTYDSVSDGAFARVDVNARPTSRNRNLGGRPLKGKRD
>DDSQRSSLMMDDDGGSSEADGENSEGDVPRGGVRKAVPRMGISASTLAHSCYGTNGTA
>QRFRSIPRNNGIVTQEQT"
>             gene            complement(9155..12160)
>                             /gene="ZK377.3"
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>                             10620..10880,11425..11780,12091..12160))
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>superfamily, most
>                             similar to nerual cell adhesion proteins"
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>                             /db_xref="GI:1825711"
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